

WHAT IS CLAIMED IS:

1. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif; and
 - b) determining whether one of said variants comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

2. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, variants of a peptide epitope 8-11 amino acids in length, each variant comprising primary anchor residues of the same HLA class I binding motif;
 - b) determining whether each of said variants comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
 - c) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

3. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
 - b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and

- c) determining whether the variant of (b) comprises only conserved non-anchor residues in comparison to at least one remaining variant, thereby identifying a candidate peptide epitope.

- 4. A method for identifying a candidate peptide epitope which induces a HLA class I CTL response against variants of said peptide epitope, comprising
 - a) identifying, from a particular antigen of an infectious agent, a population of variants of a peptide epitope 8-11 amino acids in length, each peptide epitope comprising primary anchor residues of the same HLA class I binding motif;
 - b) choosing a variant selected from the group consisting of:
 - i) a variant which comprises preferred primary anchor residues of said motif; and
 - ii) a variant which occurs with high frequency within the population of variants; and
 - c) determining whether the variant of (b) comprises conserved, semi-conserved or non-conserved non-anchor residues in comparison to each of the remaining variants; and
 - d) identifying a variant which comprises only conserved non-anchor residues in comparison to at least one remaining variant.

- 5. The method of claim 1, wherein (b) comprises identifying a variant which comprises only conserved non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

- 6. The method of claim 2 or 3, wherein (c) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

- 7. The method of claim 4, wherein (d) comprises identifying a variant which comprises only conservative non-anchor residues in comparison to at least 25%, at least 50%, at least 75%, at least 80%, at least 85%, at least 90%, at least 95%, at least 97%, or at least 99% of the remaining variants.

8. The method of any of claims 1-4, wherein (a) comprises aligning the sequences of said antigens.
9. The method of claim 3 or 4, wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif.
10. The method of claim 3 or 4, wherein (b) comprises choosing a variant which occurs with high frequency within said population.
11. The method of claim 10, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
12. The method of claim 3 or 4 wherein (b) comprises choosing a variant which comprises preferred primary anchor residues of said motif and which occurs with high frequency within said population.
13. The method of claim 12, wherein (b) comprises ranking said variants by frequency of occurrence within said population.
14. The method of any of claims 1-13, wherein the identified variant comprises the fewest conserved anchor residues in comparison to each of the remaining variants.
15. The method of any of claims 1-4, wherein the remaining variants comprise 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 30, 35, 40, 45, 50, 55, 60, 65, 70, 75, 80, 85, 90, 95, 100, 110, 120, 130, 140, 150, 160, 170, 180, 190, 200, 220, 240, 260, 280, or 300 variants.
16. The method of any of claims 1-15, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus, Epstein-Barr virus, *Mycobacterium tuberculosis*, *Chlamydia*, *Candida albicans*, *Cryptococcus neoformans*, *Coccidioides spp.*, *Histoplasma spp.*, *Aspergillus fumigatis*, *Plasmodium spp.*, *Trypanosoma spp.*, *Schistosoma spp.*, and *Leishmania spp.*
17. The method of claim 16, wherein the infectious agent is selected from the group consisting of: HIV, HBV, HCV, HPV, *Plasmodium falciparum*, Influenza virus, and Dengue virus.
18. The method of claim 16, wherein the infectious agent is HIV and the antigen is selected from the group consisting of: Gag, Env, Pol, Nef, Rev, Tat, Vif, Vpr, and Vpu.

19. The method of claim 16, wherein the infectious agent is HBV and the antigen is selected from the group consisting of: Pol, Env, Core, and NS1/Env2.
20. The method of claim 16, wherein the infectious agent is HCV and the antigen is selected from the group consisting of: Core, E1, E2, NS1, NS2, NS3, NS4, and NS5.
21. The method of claim 16, wherein the infectious agent is HPV and the antigen is selected from the group consisting of: E1, E2, E3, E4, E5, E6, E7, L1, and L2.
22. The method of claim 16, wherein the infectious agent is *Plasmodium falciparum* and the antigen is selected from the group consisting of: CSP, SSP2, EXP1, LSA1.
23. The method of any claims 1-4, wherein the selected variant and the at least one remaining variant comprise different primary anchor residues of the same motif or supermotif.
24. The method of any of claims 1-4, wherein the motif or supermotif is selected from the group consisting of those in Tables 1-2.
25. The method of any of claims 1-4, wherein the conserved non-anchor residues are at any of positions 3-7 of said variant.
26. The method of any of claims 1-4, wherein the variant comprises only 1-3 conserved non-anchor residues compared to at least one remaining variant.
27. The method of any of claims 26, wherein the variant comprises only 1-2 conserved non-anchor residues compared to at least one remaining variant.
28. The method of any of claims 27, wherein the variant comprises only 1 conserved non-anchor residue compared to at least one remaining variant.
29. The method of claim 16, wherein the infectious agent is HPV, and further wherein, the HPV infectious agent is selected from the group consisting of HPV strains 16, 18, 31, 33, 45, 52, 56, and 58.
30. The method of any of claims 1-29, wherein the variants are a population of naturally occurring variants.